

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: December 27, 2001, 18:11:29 ; Search time 4492.43 Seconds
6503.779 Million cell updates/sec

Title: US-09-830-647-4

Perfect score: 2719

Sequence: aattcggacgacgactctcg.....aaaaaaaactcag 2719

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext: 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estfun:*

2: em_estnum:*

3: em_estin:*

4: em_eston:*

5: em_estpl:*

6: em_estba:*

7: em_estco:*

8: em_estov:*

9: em_htc:*

10: gb_est:*

11: gb_htc:*

12: gb_gss:*

13: gb_gssfun:*

14: em_gss_hum:*

15: em_gss_inv:*

16: em_gss_pln:*

17: em_gss_pro:*

18: em_gss_rnd:*

19: em_gss_vrt:*

20: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AL560180 LOCUS AL560180 950 bp mRNA DEFINITION AL560180 mRNA sequence. ACCESSION AL560180 VERSION AL560180.1 GI:12906394 KEYWORDS EST. SOURCE human. ORGANISM Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 950) REFERENCE Li, W.B., Grober, C., Jesse, J. and Polayes, D. AUTHORS Li, W.B., Grober, C., Jesse, J. and Polayes, D. TITLE Full-length cDNA libraries and normalization COMMENT Unpublished (2001) JOURNAL Contact: Genoscope GENOSCOPE - Centre National de Séquençage Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr. FEATURES SOURCE 1. .950 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS00c002Y2E20" /clone_libr="LTI_FLO11_BCI" /sex="male" /tissue_type="B cells from Burkitt lymphoma" /lab_host="DB110B" /note="vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen

13 686 25.2 712 11 BF793466
14 671.4 24.7 701 10 AW960753 EST72824
C 15 661.4 24.3 743 10 AT761101 w69g03.x
C 16 647 23.8 730 10 AW105287 xds9f02.x
C 17 645.4 23.7 659 10 BE613476 BE625871 602292007
C 18 639.4 23.5 927 11 BE605871
C 19 607 22.3 2338 12 AK014480 AK014480 Mus muscu
C 20 597.8 22.0 603 10 A1824033 BE886970 60153095.x
C 21 593 21.8 615 11 BE884320 BE88697 601530523
C 22 586 21.6 701 11 BG722508 BG722508 602693762
C 23 585 21.5 585 11 BG774408 BG774408 602689338
C 24 574.8 21.1 581 11 BG719249 BG719249 602669314
C 25 572 21.0 670 10 AV645569 AV645569
C 26 568.2 20.9 706 11 BI034492 BI034492 602850523
C 27 562.8 20.7 950 10 BE88697 BE88697 60153095.x
C 28 561.6 20.7 839 10 BE564084 BE564084 601348046
C 29 561 20.6 571 10 AA451820 AA451820 2x6f01.r
C 30 560.2 19.9 760 11 BF219022 BF219022 601882245
C 31 530.4 19.5 629 11 BE882668 BE882668 601511791
C 32 548.6 20.2 639 10 BE728361 BE728361 60169844
C 33 548 20.2 935 11 BG31292 BG31292 602463961
C 34 545.2 20.1 571 10 AU150504 AU150504 601530523
C 35 540.2 19.9 760 11 BE245831 BE245831 602693762
C 36 530.4 19.5 626 10 AW967974 AW967974 601882245
C 37 523.8 19.3 839 10 BE728351 BE728351 60169844
C 38 493.4 18.1 570 10 AU143969 AU143969 601348046
C 39 490.4 18.0 493 10 A152459 A152459 tJ62b12.x
C 40 488.6 18.0 626 10 BE245831 BE245831 TCBP1E31
C 41 484.2 17.8 489 10 AW967974 AW967974 601882245
C 42 478.2 17.6 557 10 A1452802 A1452802 tJ5f11.x
C 43 474 17.4 474 10 A1452802 A1452802 tJ5f11.x
C 44 470 17.3 470 10 A1217171 A1217171 qf4910.x
C 45 468.2 17.2 484 10 A1797599 A1797599 web9f04.x

ALIGNMENTS

RESULT 1

AL560180 LOCUS AL560180 950 bp mRNA DEFINITION AL560180 mRNA sequence.

ACCESSION AL560180

VERSION AL560180.1 GI:12906394

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 950)

REFERENCE Li, W.B., Grober, C., Jesse, J. and Polayes, D.

AUTHORS Li, W.B., Grober, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

GENOSCOPE - Centre National de Séquençage

Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES SOURCE

1. .950

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS00c002Y2E20"

/clone_libr="LTI_FLO11_BCI"

/sex="male"

/tissue_type="B cells from Burkitt lymphoma"

/lab_host="DB110B"

/note="vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen

TTAGGACGAATAGAAAAGAAATCTGGACCAATGCTGAATTTGATAAAGAAGCTGAA 385
ttttatcacaaagaagaaacaaacaaatgttgttccacggttatgtttttactactgt 2319
TTTATTCACAGAGAAGAACAGATTTGTTAGTGTACCGGTAGCTTACTAGCTG 325

(whole λ - R, C, G, O1 G and "O1 G", S, O1 T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library.

ORIGIN QUERY Match $\text{similarity} \geq 0.7$; $\text{score} \geq 3.7 \pm 0.3$; DB_11 ; Length 821;

Db	481	CATTAGTCACCAAGACAGCAGTGTTAAGAGAGAAATTATAGTGAAAGCTA	540
Qy	957	tcaaggacatattttatccctcaatagatattatccaaatggc-ttgtatggta	1015

QY	1016	gtaaaattttccatattgatgata-cattaga-tactacatggaaaaaaaaggtt	1074
Db	601	GTA AA AT T C T C A T A T G A C C T T G A T A C T A C T A G A C A A G T G	659

FEATURES	source	Location/Qualifiers
1.	821	Location: "Homo sapiens"
		Db 660 GTATTACTAAGAAATCAGTACTTCAGTAGAGATGGGGAAAGAGTGG 717

"Lab.host="DH10B ("T1 phage-resistant",
note: human: lung; vector: PDR-LIB (Clontech); Site_1:
SfiI (ggccgcctggcc); Site_2: SfI (ggccatggcc);
double stranded cDNA was prepared from cell line RNA. 5
and 3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGGCTGAGGCGGCCGAC-3' and 3' adaptor
sequence: 5'-ATTCGAGAAGGCGGCCGAC-3'; dt(30)BR-1

Search completed: December 27, 2001, 18:11:44
Job time: 4699 sec